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Clinical and molecular genetics of patients with the Carney–Stratakis syndrome and germline mutations of the genes coding for the succinate dehydrogenase subunits *SDHB*, *SDHC*, and *SDHD*

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Gastrointestinal stromal tumors (GISTs) may be caused by germline mutations of the *KIT* and platelet-derived growth factor receptor- α (*PDGFRA*) genes and treated by Imatinib mesylate (STI571) or other protein tyrosine kinase inhibitors. However, not all GISTs harbor these genetic defects and several do not respond to STI571 suggesting that other molecular mechanisms may be implicated in GIST pathogenesis. In a subset of patients with GISTs, the lesions are associated with paragangliomas; the condition is familial and transmitted as an autosomal-dominant trait. We investigated 11 patients with the dyad of 'paraganglioma and gastric stromal sarcoma'; in eight (from seven unrelated families), the GISTs were caused by germline mutations of the genes encoding subunits B, C, or D (the *SDHB*, *SDHC* and *SDHD* genes, respectively). In this report, we present the molecular effects of these mutations on these genes and the clinical information on the patients. We conclude that succinate dehydrogenase deficiency may be the

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cause of a subgroup of GISTs and this offers a therapeutic target for GISTs that may not respond to STI571 and its analogs.

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Introduction

Gastrointestinal stromal tumors (GIST) may be sporadic or inherited in an autosomal-dominant manner either alone or as a component of a syndrome associated with other manifestations or predisposing to the development of multiple tumors.¹ Recently, we described 12 young patients (seven male and five female with an average age of 23 years) from five unrelated families who had both GIST and paraganglioma; the tumors were inherited in an apparently autosomal-dominant manner, with incomplete penetrance.² GISTs in these patients were multifocal and paragangliomas multicentric, supporting a genetic link between the two lesions. The condition has been referred to as the dyad of 'paraganglioma and gastric stromal sarcoma' or the 'Carney–Stratakis syndrome' or Carney–Stratakis dyad.³

Germline mutations of the genes encoding succinate dehydrogenase subunits B, C and D (*SDHB*, *SDHC* and *SDHD*) had been described in inherited paraganglioma and pheochromocytoma^{4–8} but not in familial GISTs, until patients with the dyad were studied.⁹ In this report, we

describe the molecular and clinical effects of germline *SDHB*, *SDHC* and *SDHD* mutations in patients with the dyad and their tumors. Allelic losses around the *SDHB* and *SDHC* chromosomal loci were found in GISTs from these patients, pointing to a tumor-suppressor function of the succinate dehydrogenase subunits. These tumors did not exhibit the *KIT* or platelet-derived growth factor receptor- α (*PDGFRA*) gene mutations associated with GISTs and related lesions^{10–12} that are responsive to Imatinib mesylate (STI571) and its analogs.

Methods

Clinical studies and tissue samples

The Institutional Review Boards of the participating institutions have approved the DNA and other studies of this investigation. Families with the dyad have been described by Carney and Stratakis² (Table 1). All patients had GIST or paraganglioma diagnosed by standard clinical and pathological criteria. Blood and tissue samples were collected from patients after informed consent, as

Table 1 Clinical and molecular genetics of patients with the dyad of 'paraganglioma and gastric stromal sarcoma'

Family/patient	Sex	Age ^a	Clinical manifestations; family Hx	Gene	Mutation
1/1. CTRS35	M	37	GIST; mother with pheochromocytoma	<i>SDHB</i>	IVS1+1G>T
2. CTR02 ^b					
2/2. PGL146001	M	12	PGL; one of twin brothers	<i>SDHB</i>	IVS4+1G>C
2/3. PGL146002	M	12	GIST; one of twin brothers	<i>SDHB</i>	IVS4+1G>C
3/4. B8893/T8231	F	26	GIST; multiple PGLs; father with mutation died of lung cancer at the age of 75	<i>SDHB</i>	c.45_46insCC
4/5. PGL214	F	29	GIST; PGL; unknown family Hx	<i>SDHC</i>	c.43C>T
5/6. CTRS8	F	20	GIST; PGL; mother is an unaffected carrier of the same mutation	<i>SDHC</i>	IVS5+1G>A
6/7. SDH9/04:MB 00205	M	19	GIST; multiple PGLs; pheochromocytoma; unknown family Hx	<i>SDHD</i>	c.57delG
7/8. CTRS20 ^c	M	9	GIST; multiple PGLs; mother with PGL	<i>SDHB</i>	Large deletion
8. CTRS1/3 ^c					
8/9. CTRS.1	F	20	Multiple PGLs; sister of CTRS.3		None ^d
8/10. CTRS.3	M	15	GIST; multiple PGLs		None ^d
9/11. CTRS18 ^c	M	19	GIST; multiple PGLs; two brothers with PGLs		None ^d

F, female; GIST, gastrointestinal stromal tumor; Hx, history; M, male; PGL, paraganglioma.

^aThis is the age at the time of presentation.

^bFamily CTR02 has been reported by Boccon-Gibod *et al*¹⁷.

^cKindreds CTRS20, CTRS1/3 and CTRS18 have been reported by Carney and Stratakis²; they are individual IV.4 in family 4, IV.1 and IV.4 in family 1, and III.2 in family 3, respectively.

^dNo mutations or large deletions were identified in the coding regions of the *SDHA*, *SDHB*, *SDHC* and *SDHD* genes.

described elsewhere.¹³ When possible, tissue was collected at surgery and processed for routine histopathology and immunohistochemistry following formalin fixation and paraffin embedment; additional fragments were frozen at -70°C . The antibodies for c-KIT, actin, desmin and vimentin were used at dilutions 1/1000, 1/1000, 1/200 and 1/500, respectively, and were obtained from DAKO (Carpinteria, CA, USA); the antibody for CD34 was used at a dilution of 1/100 and was obtained from BD Biosciences (San Jose, CA, USA); and the antibody for chromogranin A was diluted at 1/500 and was obtained from Chemicon (Temecula, CA, USA); for all the detection system was polymer based.

DNA was extracted from blood, frozen and archived tissue samples or cell lines using standard methods (Qiagen, Valencia, CA, USA). Tumor samples were micro-dissected from associated normal tissues.

Sequencing and allelic heterozygosity analysis

Mutation analysis for exons, exon–intron boundaries and flanking intronic regions was performed for the *KIT*, *SDHA*, *SDHB*, *SDHC*, *SDHD* and *PDGFRA* genes; polymerase chain reaction (PCR) was performed using Qiagen HotStarTaq kit (Qiagen) and primers that have been described elsewhere.^{5,6,8–12,14,15} An aliquot of the PCR product was purified with exonuclease I/shrimp alkaline phosphatase treatment (New England Biolabs, Beverly, MA, USA/USB Corporation, Cleveland, OH, USA). The purified amplicons were directly sequenced using Big-Dye Terminator v. 20 Cycle Sequencing kit (Applied Biosystems, Foster City, CA, USA) and analyzed on an ABI 3730 DNA analyzer (Applied Biosystems). Cell lines, blood cells or frozen tumor material were used for total RNA extraction, complementary DNA (cDNA) synthesis by reverse transcriptase PCR and sequencing, using appropriate transcribed sequence-based primers.

Tumor and DNA from other samples were also subjected to loss-of-heterozygosity (LOH) analysis using markers surrounding the genes in which mutations were identified (*SDHB* and *SDHC*, see below). Markers were selected using NCBI MapViewer35 (<http://www.ncbi.nlm.nih.gov/mapview/>); for each gene, at least 10 informative sequences were selected for heterozygosity studies, as described previously.¹³

For paternity and/or homozygosity testing (the latter for the twin brothers of family CTR02, see below), seven fluorescent polymorphic microsatellite markers located in three different chromosomes were used: they included *D1S159S*, *D1S2624*, *D11S934*, *D11S968*, *D14S264*, *D14S283* and *D14S990*, which were amplified and run using standard procedures.

All sequence variants that were identified in the study patients were also searched for in more than 100 ethnically matched-control DNA samples. The mutations we report were not found in any of the control samples; numerous polymorphisms were identified in the samples of the study

patients for all six genes that, however, were also present in the control samples (data not shown).

Search for microdeletions of *SDHB*, *SDHC* and *SDHD* and other loci

Tumor DNA was hybridized to Illumina (Illumina Inc., San Diego, CA, USA) HumanHap300-Duo Genotyping Bead-Chips, according to the manufacturer's protocol (www.illumina.com). Data analysis was performed using Illumina software BeadStudio (version 2) and R version 2.3 (R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria) (data not shown). For the single patient in whom *SDHB* was deleted (CTRS20; Table 1), confirmation of the hemizygous deletion was performed with semi-quantitative duplex PCR of each *SDHB* exon compared to the housekeeping *GAPDH* exon 8 gene sequence using a method that we have reported elsewhere.¹⁶ For the experiments reported here, 20 ng of genomic DNA was used as template for each semi-quantitative PCR reaction with primers flanking each *SDHB* exon and those of *GAPDH* exon 8 (Table 2) using Qiagen HotStartTaq kit (Qiagen) and 30 cycles with an annealing temperature of 55°C .

Results

Germline and tumor DNA studies

We accrued a total of nine families with the Carney–Stratakis dyad of ‘paraganglioma and gastric stromal sarcoma’ (Figures 1 and 2) from the United States, France and Italy. None had mutations of the *PDGFRA* or *KIT* genes (data not shown); however, seven probands had a mutation or a deletion in one of the three succinate

Table 2 Primers used in *SDHB* deletion analysis (case CTRS.20)^a

Gene	Amplicon	Primers
<i>GAPDH</i>	Exon 8	F: GTCACTGGTGGACCTGACCT R: TCGCTGTTGAAGTCAGAGGA
<i>SDHB</i>	Exon 1	F: GAAGCCGCCTCCCACTTG R: GCTTTCCTGACTTTTCCC
	Exon 2	F: TCTGTTGTGCCAGCAAAATG R: GCCTTCCAAGGATGTGAAAA
	Exon 3	F: ACATCCAGGTGTCTCCGATT R: CTATCAGCTTTGGCCAGC
	Exon 4	F: GTCACTGCTGTCCCCTGAT R: TGCAATAAAAAACAAACCA
	Exon 5	F: GCTGAGGTGATGATGGAATCT R: CCACACTCCTGGCAATCATC
	Exon 6	F: ATGCACTGACCCCAAAGGTA R: CAGCAATCTATTGTCTCTTG
	Exon 7	F: CTTTCCTCTGCACTCCAGA R: TTGTGAGCACATGCTACTTC
	Exon 8	F: GGAAGGAGTTTACCCCAAGA R: TGCTGTATTCATGGAAAACCA

F, forward; R, reverse.

^aSee Figure 7.

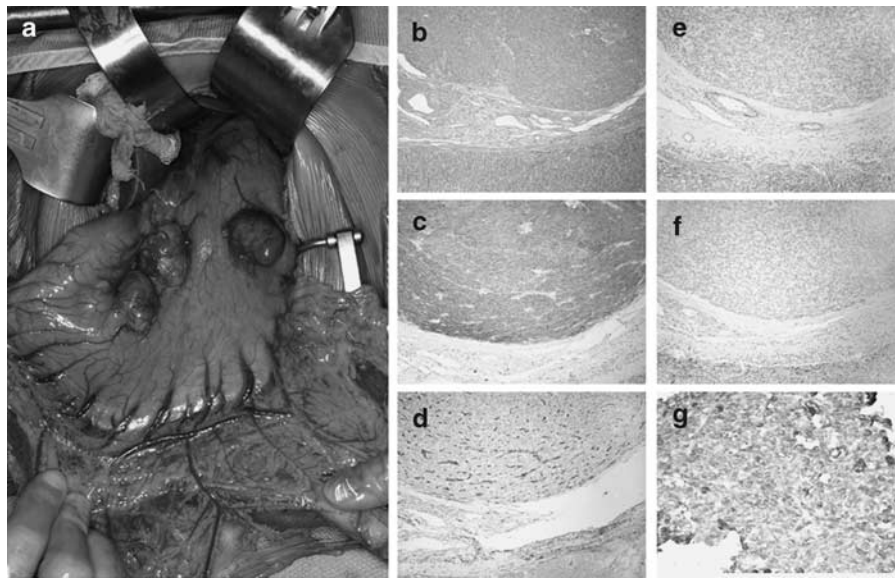


Figure 1 (a) Multiple tumors protrude from the anterior wall of stomach of patient CTRS35; two show surface bosselation. (b) Hematoxylin and eosin staining of one of the stomach GISTs from the CTRS35 patient; staining with (c) cKIT, (d) CD-34, (e) actin, (f) desmin and (g) vimentin.

dehydrogenase subunit-encoding genes (*SDHB*, *SDHC* or *SDHD*). The genomic DNA mutations have been published elsewhere.⁹ In this article, we report the clinical information of the patients and study the effects of these mutations on the transcribed message and/or tumors. There were no mutations in the coding sequence of the *SDHA* gene; a number of *SDHA* sequence variants were identified in the study patients but they were present in similar frequency in the control DNA (data not shown).

There were mutations in the *SDHB* gene in three families: in the first family, a 37-year-old male (CTRS35) had melena resulting from ulceration of a stomach GIST (Figure 1). During workup for metastatic disease, a non-functioning paraortic paraganglioma was found (Figure 2). The patient carried a relatively frequent germline mutation in intron 1 of the *SDHB* gene (IVS1 + 1 G>T or c.72 + 1G>T);^{5,9,14} cDNA analysis from his white blood cells revealed the heterozygous presence of an aberrant transcript that, when sequenced, indicated that the first part of intron 1 was transcribed (Figure 3) with the frameshift resulting in a stop codon in the middle of exon 2 and predicting a significantly truncated protein. The patient's GIST contained the mutant *SDHB* sequence only (Supplementary Figure 1), indicating loss of the normal *SDHB* allele. The patient's mother was operated for a pheochromocytoma at the age of 57; her DNA was not available.

In the second family (CTR02), monozygotic twin brothers were diagnosed with the Carney–Stratakis syndrome;¹⁷ one was operated at 12 years of age for a non-functioning paraganglioma of the organ of Zuckerkandl, and the other for a stomach GIST at age 13 years. Monozygosity was confirmed by polymorphic micro-

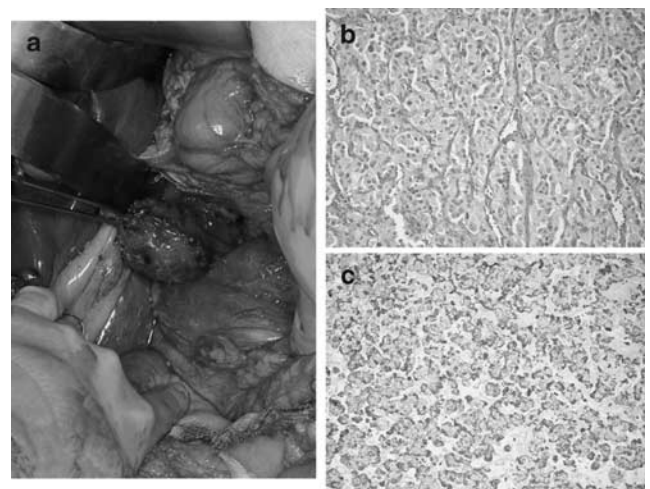


Figure 2 (a) Retroperitoneal paraganglioma with dilated veins on its surface from patient CTRS35; (b) hematoxylin and eosin staining of the paraganglioma excised from patient CTRS35; and (c) staining with the neuroendocrine marker chromogranin A.

satellite markers: the twins shared identical haplotypes (Table 3). Both carried a rare germline splice site mutation (IVS4 + 1G>C or c.423 + 1G>C) in intron 4 of the *SDHB* gene.⁴ Analysis of the cDNA from lymphocytes of one of the brothers showed that the last 18 codons of exon 4 were spliced out (Figure 4), predicting a shorter *SDHB* protein. This mutation was also present in the patients' mother and a sister; both had negative examinations for GIST and paraganglioma.

In the third kindred (B8893/T8231), the proband, now 50 years of age, had a para-aortic paraganglioma and a

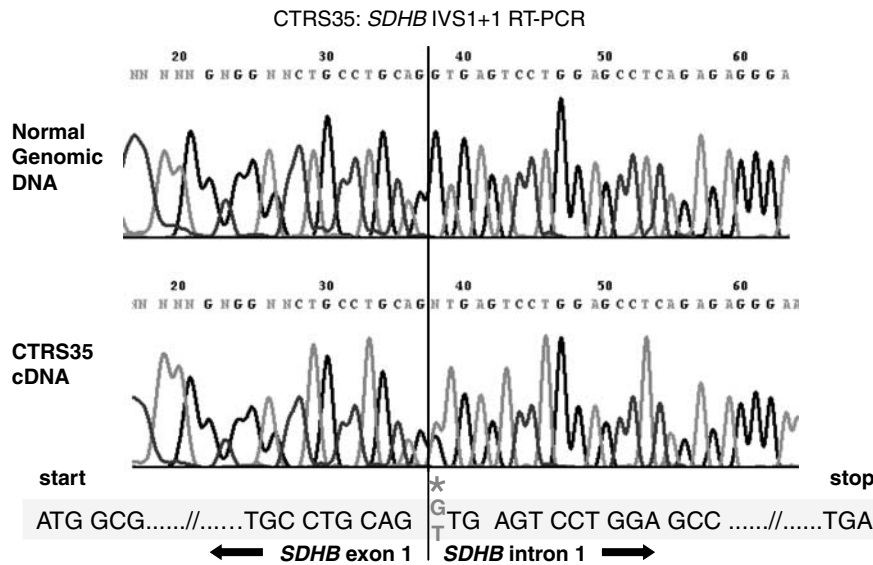


Figure 3 cDNA studies (RT-PCR) of the CTRS35 *SDHB* IVS1 + 1 mutation (*): it caused intron 1 to be transcribed, resulting in a predicted truncated protein with a stop codon coded by a downstream sequence (318 bp) of intron 1.

Table 3 Genotyping of identical twin brothers (family CTR02, individuals PGL146001 and PGL146002)^a

	PGL146001	PGL 146002
D1S1595	202/208	202/208
D1S2624	286/286	286/286
D11S934	178/180	178/180
D11S968	142/146	142/146
D14S264	220/228	220/228
D14S283	134/142	134/142
D14S990	140/154	140/154

^aGenotyping of seven fluorescent markers located in chromosomes 1, 11 and 14 in germline DNA. Following amplification, the amplicons were subjected to electrophoresis and analyzed with an ABI 3700 instrument. The data are given in base pairs.

stomach GIST. At age 26 years, she had severe hypertension and increased urinary content of catecholamines and vanillylmandelic acid. A left nephrectomy and adrenalectomy was performed. The resected specimen included three extra-adrenal paragangliomas. The patient had a novel germline 45_46insCC mutation in exon 1 of the *SDHB* gene that caused a frameshift and premature termination at codon 76 of the predicted *SDHB* protein. Allelic marker analysis suggested loss of the *SDHB* wild-type allele in both the GIST and the paraganglioma from the proband (Figure 5). The proband inherited the mutation from her father who died at the age of 75 years from a poorly differentiated lung adenocarcinoma associated with lung and pleura fibrosis and silicosis: the *SDHB* mutation was present in the father's normal lung tissue (data not shown).

There were two mutations in the *SDHC* and one in the *SDHD* genes. In the fourth family, the proband was a 29-year-old woman (PGL214) who was operated for a pancreatic, non-functional paraganglioma and, a year later, for a large retroperitoneal GIST. A novel, germline nonsense mutation in the *SDHC* gene (c.43C>T; p. Arg15X) was found.⁹ The activity of the succinate dehydrogenase-dependent SCCR in the GIST of the proband was significantly decreased with normal COX and QCCR activities;⁹ there was loss of the wild-type *SDHC* sequence (data not shown), demonstrating (for the first time in a GIST and, indeed, in any tumor) that ablation of *SDHC* can cause a severe reduction of succinate dehydrogenase activity.

In the fifth family, the proband (CTRS8), a 20-year-old female, had a gastric GIST and a non-functioning, abdominal, extra-adrenal paraganglioma; she had a rare germline intronic mutation in the *SDHC* gene (IVS5 + 1G>A or c.405 + 1G>A).⁶ cDNA analysis revealed the transcriptional effect of this splice-site substitution: the mutant allele resulted in a sequence in which exon 5 was spliced out (Figure 6), resulting in a frameshift and a stop codon in the 3' untranslated region of the gene. More than 75% of the patient's GIST cells showed allelic losses of the *SDHC* gene locus,⁹ although the normal sequence was still detectable in the chromatograms (data not shown). The patient inherited the mutation from her apparently clinically healthy 50-year-old mother.

In the sixth family, the proband (SDH9/04:MB00205) was a 19-year-old male patient who presented with melena from a stomach GIST. At age 21, the patient had a right carotid body tumor and a left adrenal pheochromocytoma;

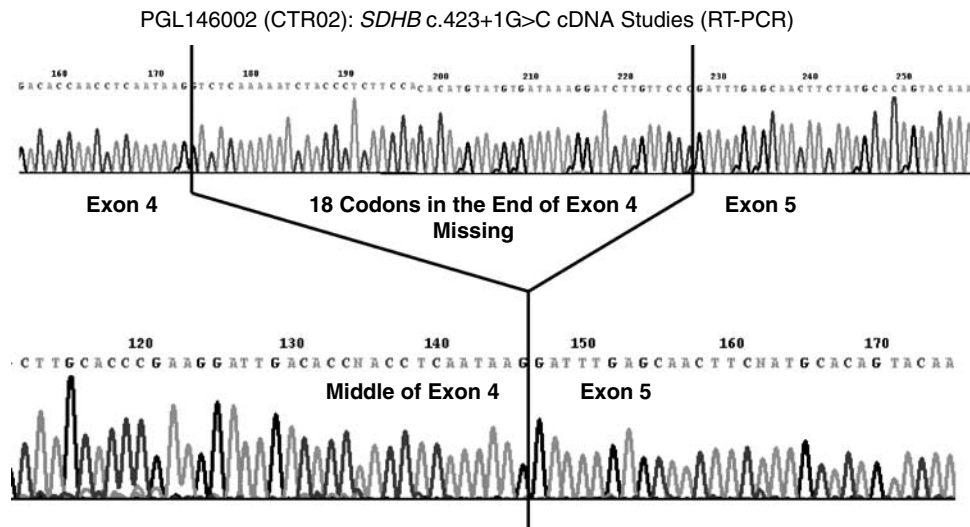


Figure 4 cDNA studies (RT-PCR) of the PGL146002 (family CTR02) *SDHB* c.423+1G>C mutation; the predicted protein was shorter but remained in frame.

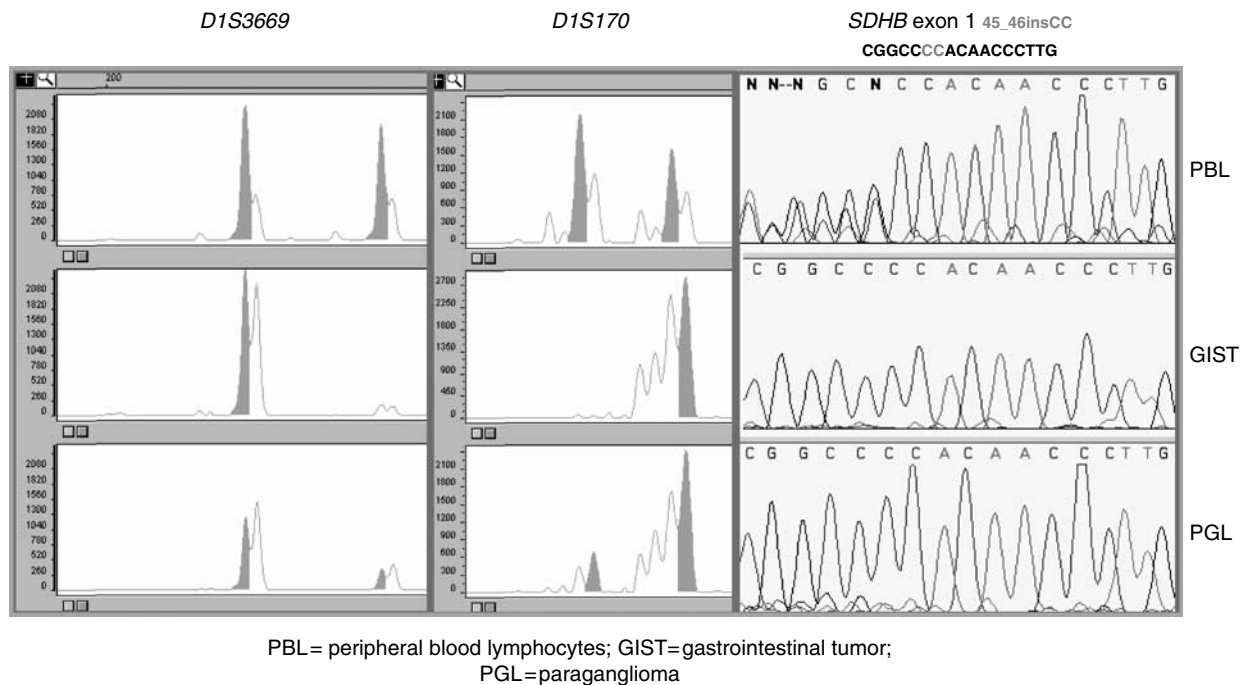


Figure 5 Loss-of-heterozygosity analysis revealed loss of the *SDHB* normal allele (the haplotypes segregating with the non-mutant allele were confirmed by analysis of multiple family members) in both a GIST and a para-aortic paraganglioma from patient B8893/T8231.

a left glomus jugular tumor was excised a year later. At age 32 he presented with metastatic paraganglioma. Sequencing of germline DNA for the genes encoding succinate dehydrogenase subunits showed a novel germline deletion of a single base at nucleotide 57 of the *SDHD* gene (c.57delG).⁹ The mutation resulted in shift in the predicted translation frame of the encoded mRNA from codon 20 to a premature stop codon at position 85. There was no tumor

DNA from this patient available; although his lesions were reported to be metastatic, we were not able to prove that genetically.

Because coding sequence mutations were not identified by sequencing the *SDHB*, *SDHC* and *SDHD* genes in the remaining three families, their DNA was also searched for deletions of the respective genes and/or their loci. This analysis revealed a large germline *SDHB* gene deletion

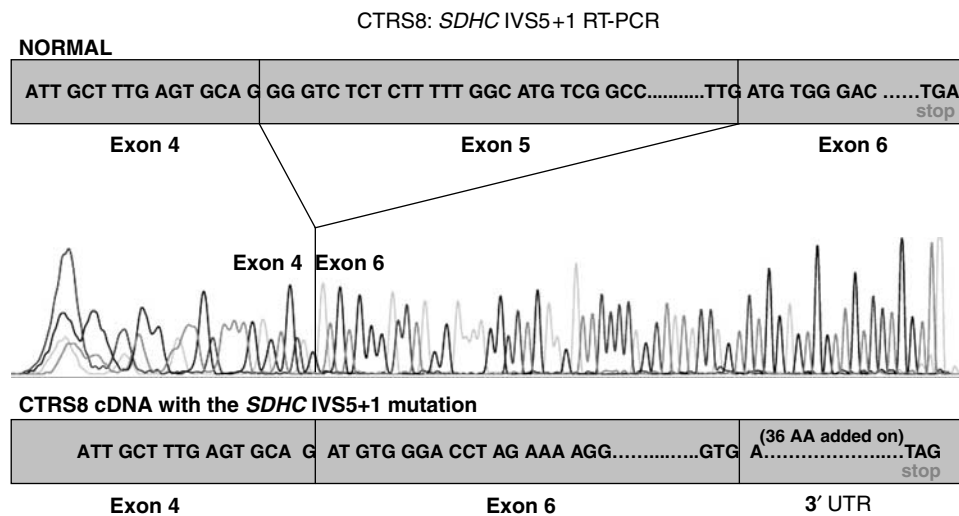


Figure 6 cDNA studies (RT-PCR) of the CTRS8 *SDHC* IVS5 + 1G>A mutation: the out-of-frame exon 6 translated directly after exon 4 sequence would predict a stop codon after 36 amino-acids coded by the 3' region of the *SDHC* gene.

(Figure 7) in another patient who first presented at the age of 9 years with multiple GISTs, and at age 16 had multiple, retroperitoneal paragangliomas. His mother had a paraganglioma but no other information or tumor DNA was available.

Additional LOH studies

The above studies documented *SDHB* and *SDHC* allelic losses in all the tumors that had mutations in the respective genes and were available for study (families 1–6), suggesting that these gene defects act in a recessive manner. Four paragangliomas and three GISTs were studied from these families; Supplementary Figure 1 shows the DNA of the tumor showing only the mutant *SDHB* sequence. Similarly, Figure 5 shows consistent *SDHB* locus losses in samples (a GIST and a paraganglioma) from the third family. Figure 8a shows loss of the *SDHC* normal allele in tumor samples from a GIST from the proband of the fifth family. In a recent study, we also showed *SDHC* mutations and allelic losses that were accompanied by deficient mitochondrial respiratory chain function in family PGL214.⁹

Finally, we also examined GISTs from other patients collected from our consortium that did not have *SDHB* and *SDHC* mutations for losses at the loci of these genes; the frequency of *SDHB* and *SDHC* loci losses among 22 tumors (10 GISTs, 10 PGLs and 2 other) ranged between 27 and 40% (Figure 8b). Although we did not investigate the *SDHD* locus, these data are consistent with those of others for sporadic paragangliomas; GISTs have not been investigated for the respective loci, but both chromosomes 1 and 11 are among those that are frequently reported as altered in genetic investigations by comparative genomic hybridization.¹⁸

Discussion

Although rare, GISTs are the most common intramural mesenchymal tumors of the gastrointestinal tract (5000 new cases/year in the United States).¹⁸ Median age at diagnosis is around 60 years; the overall 5-year survival is 40% on large tumors with high mitotic index.^{18–20} However, GISTs in children or young adults tend to be clinically different and are often part of familial syndromes.^{18,20} GISTs originate from stem cells with characteristics of the interstitial cells of Cajal (ICCs), the pacemaker cells which regulate peristalsis in the digestive tract.¹⁹ In common with ICCs, up to 95% of GISTs express the receptor tyrosine kinase KIT (CD117) and the hematopoietic progenitor cell antigen marker CD34.¹⁹ About 75–80% and 7% of GISTs harbor somatic gain-of-function mutations in the *KIT* gene¹⁰ and in the functionally related *PDGFRA* gene,^{20,21} respectively.

Germline missense mutations or small in-frame deletions of the *KIT* or *PDGFRA* genes cause most familial cases of GIST: to date, germline mutations in these genes have been identified in more than 14 families.^{1,10–12} GISTs in these families are characterized by development at multiple primary sites and presentation at a median age of 46 years; polyclonal diffuse hyperplasia of ICCs within the myenteric plexus is considered the primary effect of *KIT* constitutive activation.^{10,22,23} Other abnormalities may be present in patients with familial GISTs: for example, patients with germline *KIT* exon 11 mutations often show cutaneous hyperpigmentation in the perineum, face, neck, digits, axillae, groin and knees and less frequently urticaria pigmentosa or diffuse cutaneous mastocytosis in infancy.^{10,23} Patients with germline *PDGFRA* mutations present with multiple gastric GISTs or the condition known as intestinal neurofibromatosis.^{11,12}

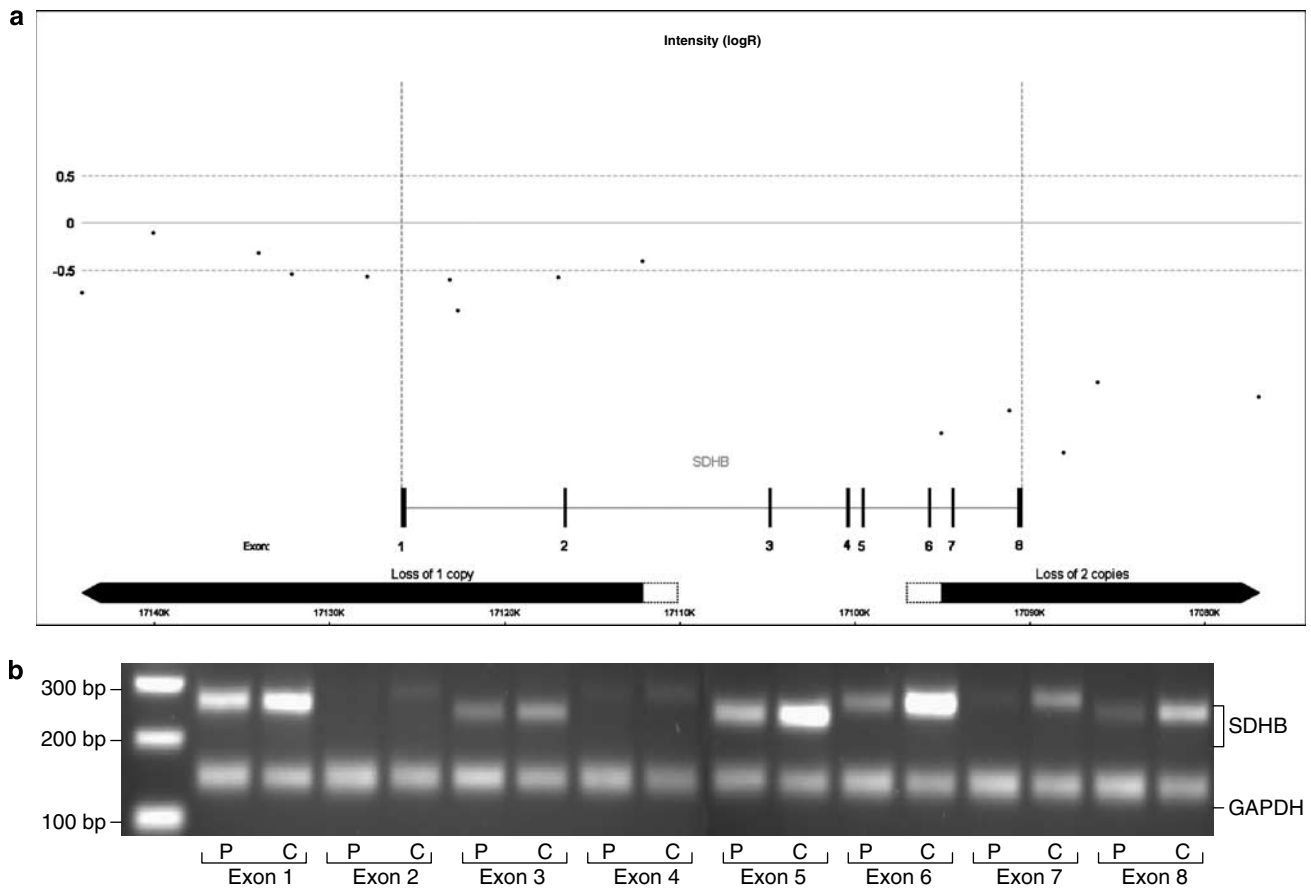


Figure 7 (a) SNP intensity in the *SDHB* region. The value is a normalized ratio in a log2 scale (-0.5 corresponds to loss deletion of one allele). (b) Semi-quantitative duplex PCR of *SDHB* exons compared to *GAPDH* exon 8.

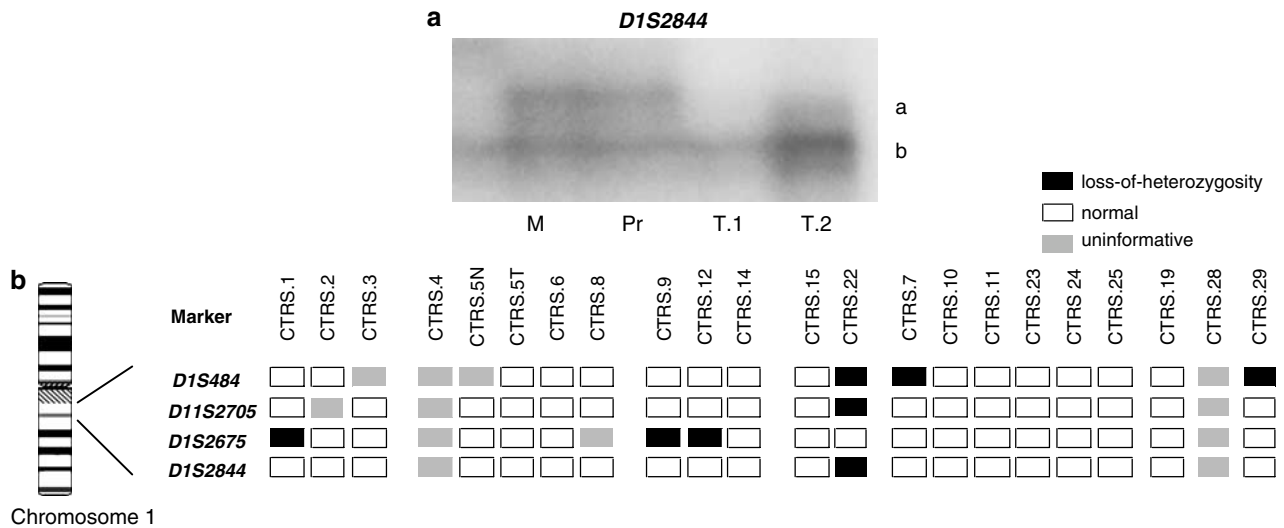


Figure 8 (a) Loss of the normal allele of the chromosome 1 *SDHC* locus in a GIST from CTRS8; the mother and the patient, who are both carriers of the *SDHC* IVS5 + 1G>A mutation are heterozygotes for the *D1S844* a and b alleles, whereas the two tumor samples have retained the b allele. (b) *SDHC* locus losses among 22 tumors with no *SDHC* mutations from patients with Carney triad and related conditions: 27% (6/22) of the tumors show at least one allelic marker loss in the vicinity of the *SDHC* gene.

Mutations in *KIT* and *PDGFRA*, either somatic or germline, are mutually exclusive events which result in the activation of common signaling pathways including the PI3K/AKT anti-apoptotic, JAK/STAT3 transcriptional and Ras/MAPK mitogenic pathways that respond to STI571 and its analogs.^{10,21,23} The existence of GISTs that lack detectable somatic mutations in either *KIT* or *PDGFRA* suggests that a different signaling pathway of tumorigenesis may be involved in the pathogenesis of these neoplasms.

Here we studied the identified germline loss-of-function mutations in the *SDHB*, *SDHC* and *SDHD* genes⁹ in patients having a recently described familial syndrome known as the dyad of ‘paraganglioma and gastric stromal sarcoma’,² referred to as the ‘Carney–Stratakis syndrome’.³ The patients presented at a young age (median age 19 years; Table 1). Their tumors displayed losses of the normal allele of the succinate dehydrogenase subunit genes and they (or their relatives) also had paragangliomas, often at multiple sites,^{2,7,9,17} which prompted us to investigate the sequence of the succinate dehydrogenase subunit genes in germline DNA from these patients.

Three of the mutations we identified had been described before in sporadic or familial pheochromocytomas or extra-adrenal paragangliomas^{4–6,8,14} (Table 4). A I127S missense mutation of the *SDHB* gene in a patient with a paraganglioma, who had a family history of paragangliomas, pheochromocytoma and whose maternal grandfather reportedly had a GIST, was also recently described.⁷ A review of the reported *SDHB* genetic changes and the ones described here does not reveal an obvious genotype–phenotype correlation

(Table 4); however, *SDHC* mutations are generally rare and have only been found in head and neck paragangliomas.⁶ Our two patients with *SDHC* mutations and the dyad (PGL214 and CTRS8) are the first cases with abdominal paragangliomas caused by mutations of this gene.

In one case, we had twins presenting one with a GIST and another with a paraganglioma (family CTR02, extensively described in Baccon-Gibod *et al*¹⁷); although technically for each one of these two patients the diagnosis of the dyad cannot be given, the identification of a common genetic defect supports the probable diagnosis of this syndrome. This family also shows the clinical heterogeneity among our patients: in CTR02, two older patients (the mother and an older sibling) are carriers and unaffected; and from the two affected carriers, one twin had a paraganglioma and the other a GIST.

The absence of *KIT* or *PDGFRA* somatic mutations and occurrence of loss of one of the succinate dehydrogenase subunits in GISTs from patients with the dyad, suggests that a deficient mitochondrial tumor suppressor gene pathway is responsible for tumor formation and not constitutively active tyrosine kinases. Succinate dehydrogenase is thus potentially a new molecular target for STI571-unresponsive GISTs. Indeed, gene expression studies in sporadic GISTs without *KIT* or *PDGFRA* mutations revealed upregulation of genes linked to the mitochondrial tumor suppressor gene pathway including VEGF;²⁴ a known target of the HIF1 transcription factor.²⁵ As succinate dehydrogenase-dependent tumorigenesis has been associated with an increase in HIF1 α nuclear pro-

Table 4 Previously reported succinate dehydrogenase subunit gene mutations: literature reports (January 2007)

Gene	Mutation	Sequence	Cases and phenotype	Reference
<i>SDHB</i>	IVS1+1G>T	c.72+1G>T (same)	Abdominal PGL; no FHx (1 case)	Elston <i>et al</i> , <i>Int Med J</i> 2006; 36: 129 (this is case F-44 in Benn <i>et al</i> , see below)
			Abdominal and thoracic PGLs; sporadic and familial; (4 cases: F-44, F-45, F-55 and F-60)	Benn <i>et al</i> ¹⁴
			Abdominal PGLs (2 cases) sporadic; one malignant	Brouwers <i>et al</i> ⁵
<i>SDHB</i>	IVS4+1G>C	c.423+1G>C (same) c.423+1G>A (different substitution)	PGLs (1 case; no other details) PGLs (4 cases; no other details)	Amar <i>et al</i> ⁴ Amar <i>et al</i> ⁴
			Neck PGL (1 case)	Bayley <i>et al</i> , <i>BMC Med Genet</i> 2006; 7 doi:10.1186/1471-2350-7-1
<i>SDHB</i>	Gene deletion	Variable size ^a Variable size ^a	Neck PGL (1 case) Neck, abdominal PGL (1 family; BRZ01)	Cascón <i>et al</i> , <i>Genes Chrom Cancer</i> 2006; 45: 213 McWhinney <i>et al</i> ¹⁶
<i>SDHC</i>	IVS5+1G>A	c.405+1G>A	Neck PGL (2 cases, #5 and #7) Neck PGL (1 case; same as #7, above)	Schiavi <i>et al</i> ⁶ Niemann <i>et al</i> , <i>Hum Genet</i> 2003; 113: 92

PGL, paraganglioma.

^aThe three *SDHB* gene deletions (the two described so far and the one in this article) are of variable size.

tein,²⁶ it is not unreasonable to speculate that the development of non-KIT and non-PDGFR α -associated GISTs may be associated with abnormal regulation of the hypoxic or pseudo-hypoxic pathway.

In conclusion, familial GISTs may be caused by mutations of the succinate dehydrogenase subunit genes *SDHB*, *SDHC* and *SDHD*, and abdominal paragangliomas associated with GISTs may be caused uniquely by *SDHC* mutations. Although we do not recommend at this point that all patients with succinate dehydrogenase subunit mutations are screened for GISTs by imaging studies, we do suggest that a careful medical and family history regarding gastrointestinal symptoms and/or tumors should be recorded in every patient with such germline genetic defects. The present study impacts genetic counseling of patients with GISTs or paragangliomas, has implications on the understanding of GIST formation and/or progression, and may lead to new therapies for these tumors.

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